

Amendments to the Specification

Please amend the paragraph beginning at page 21, line 19 - page 22, line 17 as follows:

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the BLAST 2.0 suite of programs using default parameters. Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology-Information

[[<http://www.ncbi.nlm.nih.gov/>]](world wide web at [ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov/)). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

Please amend the paragraph beginning at page 29, lines 13-17 as follows:

Typically this region is comprised of two overlapping heat shock elements having the following sequence:

CTGGACCCCC TCTCGA GAGTTCCGCT
(SEQ ID NO:1)

At page 30, please amend Table 1 as follows:

Table 1. Engineering of Ubi-1 promoter HSE

DNA construct	DNA sequence ¹	HSE engineering	Transgenic lines
PGN7062	CTGGACCCCTCTCGAGAGTTCCGCT (SEQ ID NO:1)	wild type	GSB
PGN7547	-----	HSEs deleted	GSC
PGN7565	CTGGACCCCT<u>CTCGA</u>----- (SEQ ID NO:2)	3' HSE deleted	GSD
PGN7583	----- CTCGAGAGTTCCGCT (SEQ ID NO:3)	5' HSE deleted	GSE
PGN7600	CTGGACCCCTCTCGACTCGAGAGTTCCGCT (SEQ ID NO:4)	HSEs adjacent	GSF
PGN8926	3x(GACACGTAGAATGAGTCATCAC) (SEQ ID NO:5)	HSEs replaced by <i>Ps1 trimer</i>	GSG

¹The 5' HSE is in bold type and the 3' HSE is underlined.

At page 31, please amend Table A as follows:

TABLE A

Species	Factor	Target Gene	5' extent of site	3' extent of site	Site Sequence
Arabidopsis thaliana	EBP	Pathogenesis-related protein 1b	-207	-192	atGGGGCTtta (SEQ ID NO:6)
Arabidopsis thaliana	HY5	Ribulose-1,5-biphosphate carboxylase	-241	-230	CTTCCACGTGGCA (SEQ ID NO:7)
Hordeum vulgare	BLZ-1	B-hordein	-252	-220	acatggaaatggatataatggGTGAGTC (SEQ ID NO:8)
Hordeum vulgare	Gamyb	High-pI alpha-amylase	-149	-128	ggccgatAACAAACtccggccg (SEQ ID NO:9)
an Oryza sativa virus	RF2a	Rice tungro bacilliform virus promoter	-53	-39	CCAGTGCCCCCTTG (SEQ ID NO:10)
Phaseolus vulgaris	ROM1	Phytohemagglutinin	-207	-199	GCCACGTCA
Pisum sativum	GT-1	Ribulose-1,5-biphosphate carboxylase	-257	-245	GATTTACACT (SEQ ID NO:11)
Triticum aestivum	SPA	Low molecular weight glutenin-1D1	-256	-241	ttaCGTGAGTCATA (SEQ ID NO:12)
Zea mays	Dof2	C4-type phosphoenolpyruvate carboxylase	-774	-765	ATACTTTTC (SEQ ID NO:13)
Zea mays	Opaque-2	22-kD Zein	-305	-288	tGTCAATTCCACGTAGAG (SEQ ID NO:14)

At page 45, line 17, please amend Table 1 as follows:

Table 1. Engineered Ubi-1 promoter HSE

DNA construct	DNA sequence ¹	Transgenic lines	
<u>description</u>			
PGN7062	CTGGACCCCTCTCGAGAGAGTTCCGCT <u>(SEQ ID NO:1)</u>	wild type	GSB
PGN7547	-----	HSEs deleted	GSC
PGN7565	CTGGACCCCTCTCGA ----- <u>(SEQ ID NO:2)</u>	3' HSE deleted	GSD
PGN7583	----- CTCGAGAGAGTTCCGCT <u>(SEQ ID NO:3)</u>	5' HSE deleted	GSE
PGN7600	CTGGACCCCTCTCGACTCGAGAGAGTTCCGCT <u>(SEQ ID NO:4)</u>	HSEs adjacent	GSF
PGN8926	3x(GACACGTAGAATGAGTCATCAC) <u>(SEQ ID NO:5)</u>	HSEs replaced by <u>PstI trimer</u>	GSG

¹The 5' HSE is in bold type and the 3' HSE is underlined.